

Amendments to the Specification

Please replace the paragraph at page 6, lines 20-21 with the following paragraph:

Figure 2 is a diagram of the BLAST derived homologies of the SIN1 protein, as follows: helicase C domains of SIN1 (SEQ ID NO: 5 and SEQ ID NO: 9) compared to yeast *DRS1* (SEQ ID NO: 4 and SEQ ID NO: 7), yeast *RRP3* (SEQ ID NO: 6), and *Drosophila Vasa* products (SEQ ID NO: 3 and SEQ ID NO: 8); RNase 3 domain of SIN1 (SEQ ID NO: 13) compared to pombe *PAC1* (SEQ ID NO: 10), *Drosophila Vasa* (SEQ ID NO: 11), and *C. elegans* YM68 product (SEQ ID NO: 12); and dsRBD domains of SIN1 (SEQ ID NO: 17 and SEQ ID NO: 18) compared to *Drosophila Stauf* products (SEQ ID NO: 14, SEQ ID NO: 15, and SEQ ID NO: 16).

Please replace the paragraph at page 20, lines 4-27 with the following paragraph:

Analysis of this protein revealed a domain structure highly suggestive of an RNA helicase (Company et al., "Requirement of the RNA Helicase-Like Protein PRP22 for Release of Messenger RNA from Spliceosomes," Nature 349:487-493 (1991); Linder et al., "Birth of the D-E-A-D Box," Nature 337:121-122 (1989); Luking et al., "The Protein Family of RNA Helicases," Crit. Rev. Biochem. Mol. Biol. 33:259-296 (1998); Martins et al., "Mutational Analysis of Vaccinia Virus Nucleoside Triphosphate Phosphohydrolase I, a DNA-Dependent ATPase of the DExH Box Family," Journal of Virology 73:1302-1308 (1999), which are hereby incorporated by reference), of which *Drosophila* maternal effect gene *Vasa* is a representative (Rongo et al., "Germplasm Assembly and Germ Cell Migration in *Drosophila*," Cold Spring Harb. Symp. Quant. Biol. 62:1-11 (1997), which is hereby incorporated by reference). Shown in the lower portion of Figure 1 is the arrangement of functional motifs of the predicted SIN1 protein: a bipartite N-terminal nuclear localization signal (NLS), an RNA helicase C domain, two RNase III catalytic domains, a PIMS (for PIWI Middle domain-SHORT INTEGUMENTS1, PIWI being a family of important plant developmental proteins) motif, and two C-terminal repeats of a dsRNA binding domain. A BLAST search yielded numerous high homology strikes of these domains, as shown in Figure 2. Each of the three functional domains is strongly conserved within its own family. For example, the helicase C motif (SEQ ID NO: 5 and SEQ ID NO: 9) shows strong similarity, among others, to yeast *RRP3* (SEQ ID NO: 6), *DRS1* (SEQ ID NO: 4 and SEQ ID

NO: 7), and fly *Vasa* products (SEQ ID NO: 3 and SEQ ID NO: 8), RNase3 domains (SEQ ID NO: 13) to pombe *PAC1* (SEQ ID NO: 10) or worm K12H4.8 (YM68) (SEQ ID NO: 12), and dsRBD domains (SEQ ID NO: 17 and SEQ ID NO: 18) to Drosophila *Staufen* products (SEQ ID NO: 14, SEQ ID NO: 15, and SEQ ID NO: 16).